

SEQUENCE LISTING

<110> Thompson, John E.
Wang, Tzann-Wei
Lu, Dongen Lilly

<120> DNA ENCODING A PLANT DEOXYHYPUSINE SYNTHASE, TRANSGENIC
PLANTS AND A METHOD FOR CONTROLLING PROGRAMMED CELL
DEATH IN PLANTS

<130> 10799/9

<140>

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<150> 09/348,675

<151> 1999-07-06

<160> 35

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Lycopersicon sp.

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<221> CDS

<222> (54..1196)

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Phe Lys Glu Ser Glu Asn Leu Glu Gly Ser Cys Thr Lys Ile Glu Gly
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Cys Lys Ile Phe Leu Gly Phe Thr Ser Asn Leu Val Ser Ser Gly Val

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 Met Val Ser Thr Gly Phe Gln Ala Ser Asn Leu Gly Asp Ala Ile Ala
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 Ile Val Asn Gln Met Leu Asp Trp Arg Leu Ser His Glu Leu Pro Thr
 65 70 75 80
 Glu Asp Cys Ser Glu Glu Glu Arg Asp Val Ala Tyr Arg Glu Ser Val
 85 90 95
 Thr Cys Lys Ile Phe Leu Gly Phe Thr Ser Asn Leu Val Ser Ser Gly
 100 105 110
 Val Arg Asp Thr Val Arg Tyr Leu Val Gln His Arg Met Val Asp Val
 115 120 125
 Val Val Thr Thr Ala Gly Gly Ile Glu Glu Asp Leu Ile Lys Cys Leu
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 Ala Pro Thr Tyr Lys Gly Asp Phe Ser Leu Pro Gly Ala Ser Leu Arg
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 Ser Lys Gly Leu Asn Arg Ile Gly Asn Leu Leu Val Pro Asn Asp Asn
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 Tyr Cys Lys Phe Glu Asn Trp Ile Ile Pro Val Phe Asp Gln Met Tyr
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 Glu Glu Gln Ile Asn Glu Lys Val Leu Trp Thr Pro Ser Lys Val Ile
 195 200 205

Ala Arg Leu Gly Lys Glu Ile Asn Asp Glu Thr Ser Tyr Leu Tyr Trp
 210 215 220

Ala Tyr Lys Asn Arg Ile Pro Val Phe Cys Pro Gly Leu Thr Asp Gly
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Ser Leu Gly Asp Met Leu Tyr Phe His Ser Phe Lys Lys Gly Asp Pro
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Asp Asn Pro Asp Leu Asn Pro Gly Leu Val Ile Asp Ile Val Gly Asp
 260 265 270

Ile Arg Ala Met Asn Gly Glu Ala Val His Ala Gly Leu Arg Lys Thr
 275 280 285

Gly Met Ile Ile Leu Gly Gly Gly Leu Pro Lys His His Val Cys Asn
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Ala Asn Met Met Arg Asn Gly Ala Asp Phe Ala Val Phe Ile Asn Thr
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Ala Gln Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala
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Val Ser Trp Gly Lys Ile Arg Gly Gly Ala Lys Thr Val Lys Val His
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Cys Asp Ala Thr Ile Ala Phe Pro Ile Leu Val Ala Glu Thr Phe Ala
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Tyr Asp Phe Asn Gln Gly Val Asp Tyr Pro Lys Leu Met Arg Ser Met
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ctc acc acc gga ttt caa gcc tcg aat ctc ggc gaa gct att gat gtc 253
Leu Thr Thr Gly Phe Gln Ala Ser Asn Leu Gly Glu Ala Ile Asp Val
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gtc aat caa atg gttcgtttct cgaattcatc aaaaataaaa attccttctt 305
Val Asn Gln Met
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Phe Glu Phe Val
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Leu Lys Leu Asp Trp Arg Leu Ala Asp Glu Thr Thr Val Ala Glu Asp
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Cys Ser Glu Glu Glu Lys Asn Pro Ser Phe Arg Glu Ser Val Lys Cys
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Lys Ile Phe Leu Gly Phe Thr Ser Asn Leu Val Ser Ser Gly Val Arg
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gat act att cgt tat ctt gtt cag cat cat atg gtttgtgatt tttgctttat 556
Asp Thr Ile Arg Tyr Leu Val Gln His His Met
120 125
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tctgcag gtt gat gtt ata gtc acg aca act ggt ggt gtt gag gaa gat 665
Val Asp Val Ile Val Thr Thr Thr Gly Gly Val Glu Glu Asp
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Val Pro Asn Asp Asn Tyr Cys Lys Phe Glu Asp Trp Ile Ile Pro Ile
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Phe Asp Glu Met Leu Lys Glu Gln Lys Glu Glu
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 Asn Val Leu Trp Thr Pro Ser Lys Leu Leu Ala Arg Leu Gly Lys Glu
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 Ile Asn Asn Glu Ser Ser Tyr Leu Tyr Trp Ala Tyr Lys
 220 225 230

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 Gly Leu Ile Ile Asp Val Val Gln
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tatcacagtg tttatggtct ttgaaccagt taatgtttta tgaaca gat atc aga 1583
 Asp Ile Arg

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 Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala Val Ser
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 Trp Gly Lys Ile Arg Gly Ser Ala Lys Thr Val Lys Val Cys Phe Leu
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00627" 6705260

Gly Gly Gly Leu Pro Lys His His Ile Cys Asn Ala Asn Met Met Arg
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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

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205			210				215						220			
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		225				230						235				
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240				245				250								
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His	Ser	Phe	Arg	Asn	Pro	Gly	Leu	Ile	Val	Asp	Val	Val	Gln	Asp	Ile	
255				260				265								
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aac atg atg aga aat ggc gcc gat tat gct gtt ttc atc aac act gcc 1203
Asn Met Met Arg Asn Gly Ala Asp Tyr Ala Val Phe Ile Asn Thr Ala
305                310                315

gaa gag ttt gac ggc agt gat tct ggt gct cgc ccc gat gag gct att 1251
Glu Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala Ile
320                325                330

tca tgg ggc aaa att agc gga tct gct aag act gtg aag gtg cat tgt 1299
Ser Trp Gly Lys Ile Ser Gly Ser Ala Lys Thr Val Lys Val His Cys
335                340                345

gat gcc acg ata gct ttc cct cta cta gtc gct gag aca ttt gca gca 1347
Asp Ala Thr Ile Ala Phe Pro Leu Leu Val Ala Glu Thr Phe Ala Ala
350                355                360

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Lys Arg Glu Lys Glu Arg Lys Ser Cys
365                370

aaaaatctgt gttatacaag tctcgaaatg cattttagta attgacttga tcttatcatt 1454

tcaatgtgtt atctttgaaa atgttggttaa tgaaacatct cacctcttct atacaacatt 1514

gttgatccat tgtactccgt atcttgtaaat tttggaaaaa aaaaaccgtc tattgttacg 1574

agagagtaca tttttgaggt aaaaatatag gatttttgtg cgatgcaaat gctggttatt 1634

cccttgaaaa aaaaaaaaaa aaaaaa 1660

<210> 10
<211> 373
<212> PRT
<213> Dianthus sp.

<220>
<223> DHS

<400> 10
Met Glu Asp Ala Asn His Asp Ser Val Ala Ser Ala His Ser Ala Ala
1                5                10                15

Phe Lys Lys Ser Glu Asn Leu Glu Gly Lys Ser Val Lys Ile Glu Gly
20                25                30

Tyr Asp Phe Asn Gln Gly Val Asn Tyr Ser Lys Leu Leu Gln Ser Phe
35                40                45

Ala Ser Asn Gly Phe Gln Ala Ser Asn Leu Gly Asp Ala Ile Glu Val
50                55                60

Val Asn His Met Leu Asp Trp Ser Leu Ala Asp Glu Ala Pro Val Asp
65                70                75                80

Asp Cys Ser Glu Glu Glu Arg Asp Pro Lys Phe Arg Glu Ser Val Lys
85                90                95

Cys Lys Val Phe Leu Gly Phe Thr Ser Asn Leu Ile Ser Ser Gly Val
100               105               110

Arg Asp Thr Ile Arg Tyr Leu Val Gln His His Met Val Asp Val Ile

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115	120	125
Val Thr Thr Thr Gly Gly Ile Glu Glu Asp Leu Ile Lys Gly Arg Ser		
130	135	140
Ile Lys Cys Leu Ala Pro Thr Phe Lys Gly Asp Phe Ala Leu Pro Gly		
145	150	155
Ala Gln Leu Arg Ser Lys Gly Leu Asn Arg Ile Gly Asn Leu Leu Val		
165	170	175
Pro Asn Asp Asn Tyr Cys Lys Phe Glu Asp Trp Ile Ile Pro Ile Leu		
180	185	190
Asp Lys Met Leu Glu Glu Gln Ile Ser Glu Lys Ile Leu Trp Thr Pro		
195	200	205
Ser Lys Leu Ile Gly Arg Leu Gly Arg Glu Ile Asn Asp Glu Ser Ser		
210	215	220
Tyr Leu Tyr Trp Ala Phe Lys Asn Asn Ile Pro Val Phe Cys Pro Gly		
225	230	235
Leu Thr Asp Gly Ser Leu Gly Asp Met Leu Tyr Phe His Ser Phe Arg		
245	250	255
Asn Pro Gly Leu Ile Val Asp Val Val Gln Asp Ile Arg Ala Val Asn		
260	265	270
Gly Glu Ala Val His Ala Ala Pro Arg Lys Thr Gly Met Ile Ile Leu		
275	280	285
Gly Gly Gly Leu Pro Lys His His Ile Cys Asn Ala Asn Met Met Arg		
290	295	300
Asn Gly Ala Asp Tyr Ala Val Phe Ile Asn Thr Ala Glu Glu Phe Asp		
305	310	315
Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala Ile Ser Trp Gly Lys		
325	330	335
Ile Ser Gly Ser Ala Lys Thr Val Lys Val His Cys Asp Ala Thr Ile		
340	345	350
Ala Phe Pro Leu Leu Val Ala Glu Thr Phe Ala Ala Lys Arg Glu Lys		
355	360	365
Glu Arg Lys Ser Cys		
370		

<210> 11
 <211> 780
 <212> DNA
 <213> Lycopersicon sp.

<220>
 <223> eif-5A

<220>
 <221> CDS
 <222> (43) .. (522)

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 Met Ser Asp Glu

gaa cac cat ttt gag tca aag gca gat gct ggt gcc tca aaa act ttc 102
 Glu His His Phe Glu Ser Lys Ala Asp Ala Gly Ala Ser Lys Thr Phe
 5 10 15 20
 cca cag caa gct gga acc atc cgt aag aat ggt tac atc gtt atc aaa 150
 Pro Gln Gln Ala Gly Thr Ile Arg Lys Asn Gly Tyr Ile Val Ile Lys
 25 30 35
 ggc cgt ccc tgc aag gtt gtt gag gtc tcc act tca aaa act gga aaa 198
 Gly Arg Pro Cys Lys Val Val Glu Val Ser Thr Ser Lys Thr Gly Lys
 40 45 50
 cac gga cat gct aaa tgt cac ttt gtg gca att gac att ttc aat gga 246
 His Gly His Ala Lys Cys His Phe Val Ala Ile Asp Ile Phe Asn Gly
 55 60 65
 aag aaa ctg gaa gat atc gtt ccg tcc tcc cac aat tgt gat gtg cca 294
 Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His Asn Cys Asp Val Pro
 70 75 80
 cat gtt aac cgt acc gac tat cag ctg att gat atc tct gaa gat ggt 342
 His Val Asn Arg Thr Asp Tyr Gln Leu Ile Asp Ile Ser Glu Asp Gly
 85 90 95 100
 ttt gtc tca ctt ctt act gaa agt gga aac acc aag gat gac ctc agg 390
 Phe Val Ser Leu Leu Thr Glu Ser Gly Asn Thr Lys Asp Asp Leu Arg
 105 110 115
 ctt ccc acc gat gaa aat ctg ctg aag cag gtt aaa gat ggg ttc cag 438
 Leu Pro Thr Asp Glu Asn Leu Leu Lys Gln Val Lys Asp Gly Phe Gln
 120 125 130
 gaa gga aag gat ctt gtg gtg tct gtt atg tct gcg atg ggc gaa gag 486
 Glu Gly Lys Asp Leu Val Val Ser Val Met Ser Ala Met Gly Glu Glu
 135 140 145
 cag att aac gcc gtt aag gat gtt ggt acc aag aat tagttatgtc 532
 Gln Ile Asn Ala Val Lys Asp Val Gly Thr Lys Asn
 150 155 160
 atggcagcat aatcactgcc aaagctttaaa gacattatca taccctaattg tgggtactttg 592
 atatcactag attataaaact gtgtttatttg cactgtttcaa aacaaaagaa agaaaactgc 652
 tggtatggct agagaaaagta ttggcttttga gcttttgaca gcacagttga actatgtgaa 712
 aattctactt tttttttttt gggtaaaata ctgctcgttt aatgttttgc aaaaaaaaaa 772
 aaaaaaaaaa 780

<210> 12
 <211> 160
 <212> PRT
 <213> Lycopersicon sp.

<220>
 <223> eif-5A

<400> 12
 Met Ser Asp Glu Glu His His Phe Glu Ser Lys Ala Asp Ala Gly Ala
 1 5 10 15
 Ser Lys Thr Phe Pro Gln Gln Ala Gly Thr Ile Arg Lys Asn Gly Tyr

20 25 30
 Ile Val Ile Lys Gly Arg Pro Cys Lys Val Val Glu Val Ser Thr Ser
 35 40 45
 Lys Thr Gly Lys His Gly His Ala Lys Cys His Phe Val Ala Ile Asp
 50 55 60
 Ile Phe Asn Gly Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His Asn
 65 70 75 80
 Cys Asp Val Pro His Val Asn Arg Thr Asp Tyr Gln Leu Ile Asp Ile
 85 90 95
 Ser Glu Asp Gly Phe Val Ser Leu Leu Thr Glu Ser Gly Asn Thr Lys
 100 105 110
 Asp Asp Leu Arg Leu Pro Thr Asp Glu Asn Leu Leu Lys Gln Val Lys
 115 120 125
 Asp Gly Phe Gln Glu Gly Lys Asp Leu Val Val Ser Val Met Ser Ala
 130 135 140
 Met Gly Glu Glu Gln Ile Asn Ala Val Lys Asp Val Gly Thr Lys Asn
 145 150 155 160

<210> 13
 <211> 812
 <212> DNA
 <213> Dianthus sp.

<220>
 <223> eif-5A
 <220>
 <221> CDS
 <222> (67)..(546)

<400> 13
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 cgaacg atg tcg gac gac gat cac cat ttc gag tca tcg gcc gac gcc 108
 Met Ser Asp Asp Asp His His Phe Glu Ser Ser Ala Asp Ala
 1 5 10
 gga gca tcc aag act tac cct caa caa gct ggt aca atc cgc aag agc 156
 Gly Ala Ser Lys Thr Tyr Pro Gln Gln Ala Gly Thr Ile Arg Lys Ser
 15 20 25 30
 ggt cac atc gtc atc aaa aat cgc cct tgc aag gtg gtt gag gtt tct 204
 Gly His Ile Val Ile Lys Asn Arg Pro Cys Lys Val Val Glu Val Ser
 35 40 45
 acc tcc aag act ggc aag cac ggt cat gcc aaa tgt cac ttt gtt gcc 252
 Thr Ser Lys Thr Gly Lys His Gly His Ala Lys Cys His Phe Val Ala
 50 55 60
 att gac att ttc aac ggc aag aag ctg gaa gat att gtc ccc tca tcc 300
 Ile Asp Ile Phe Asn Gly Lys Lys Leu Glu Asp Ile Val Pro Ser Ser
 65 70 75
 cac aat tgt gat gtt cca cat gtc aac cgt gtc gac tac cag ctg ctt 348
 His Asn Cys Asp Val Pro His Val Asn Arg Val Asp Tyr Gln Leu Leu
 80 85 90

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gat atc act gaa gat ggc ttt gtt agt ctg ctg act gac agt ggt gac 396
Asp Ile Thr Glu Asp Gly Phe Val Ser Leu Leu Thr Asp Ser Gly Asp
 95 100 105 110

acc aag gat gat ctg aag ctt cct gct gat gag gcc ctt gtg aag cag 444
Thr Lys Asp Asp Leu Lys Leu Pro Ala Asp Glu Ala Leu Val Lys Gln
 115 120 125

atg aag gag gga ttt gag gcg ggg aaa gac ttg att ctg tca gtc atg 492
Met Lys Glu Gly Phe Glu Ala Gly Lys Asp Leu Ile Leu Ser Val Met
 130 135 140

tgt gca atg gga gaa gag cag atc tgc gcc gtc aag gac gtt agt ggt 540
Cys Ala Met Gly Glu Glu Gln Ile Cys Ala Val Lys Asp Val Ser Gly
 145 150 155

ggc aag tagaagcttt tgatgaatcc aatactacgc ggtgcagttg aagcaatagt 596
Gly Lys
 160

aatctcgaga acattctgaa ccttatatgt tgaattgatg gtgcttagtt tgttttggaa 656
atctcttttgc aattaagttg taccaaataca atggatgtaa tgtcttgaat ttgttttatt 716
tttgtttttga tgtttgctgt gattgcatta tgcattgtta tgagttatga cctgtttataa 776
cacaaggttt tggtaaaaaa aaaaaaaaaa aaaaaa 812

<210> 14
<211> 160
<212> PRT
<213> Dianthus sp.

<220>
<223> eif-5A

<400> 14
Met Ser Asp Asp Asp His His Phe Glu Ser Ser Ala Asp Ala Gly Ala
 1 5 10 15

Ser Lys Thr Tyr Pro Gln Gln Ala Gly Thr Ile Arg Lys Ser Gly His
 20 25 30

Ile Val Ile Lys Asn Arg Pro Cys Lys Val Val Glu Val Ser Thr Ser
 35 40 45

Lys Thr Gly Lys His Gly His Ala Lys Cys His Phe Val Ala Ile Asp
 50 55 60

Ile Phe Asn Gly Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His Asn
 65 70 75 80

Cys Asp Val Pro His Val Asn Arg Val Asp Tyr Gln Leu Leu Asp Ile
 85 90 95

Thr Glu Asp Gly Phe Val Ser Leu Leu Thr Asp Ser Gly Asp Thr Lys
 100 105 110

Asp Asp Leu Lys Leu Pro Ala Asp Glu Ala Leu Val Lys Gln Met Lys
 115 120 125

Glu Gly Phe Glu Ala Gly Lys Asp Leu Ile Leu Ser Val Met Cys Ala
 130 135 140

Met Gly Glu Glu Gln Ile Cys Ala Val Lys Asp Val Ser Gly Gly Lys

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145

150

155

160

<210> 15
<211> 702
<212> DNA
<213> Arabidopsis sp.

<220>
<223> eif-5A

<220>
<221> CDS
<222> (56)..(529)

<400> 15
ctgttaccaa aaaatctgta ccgcaaaatc ctcgtcgaag ctcgctgctg caacc atg 58
Met
1

tcc gac gag gag cat cac ttt gag tcc agt gac gcc gga gcg tcc aaa 106
Ser Asp Glu Glu His His Phe Glu Ser Ser Asp Ala Gly Ala Ser Lys
5 10 15

acc tac cct caa caa gct gga acc atc cgt aag aat ggt tac atc gtc 154
Thr Tyr Pro Gln Gln Ala Gly Thr Ile Arg Lys Asn Gly Tyr Ile Val
20 25 30

atc aaa aat cgt ccc tgc aag gtt gtt gag gtt tca acc tcg aag act 202
Ile Lys Asn Arg Pro Cys Lys Val Val Glu Val Ser Thr Ser Lys Thr
35 40 45

ggc aag cat ggt cat gct aaa tgt cat ttt gta gct att gat atc ttc 250
Gly Lys His Gly His Ala Lys Cys His Phe Val Ala Ile Asp Ile Phe
50 55 60 65

acc agc aag aaa ctc gaa gat att gtt cct tct tcc cac aat tgt gat 298
Thr Ser Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His Asn Cys Asp
70 75 80

gtt cct cat gtc aac cgt act gat tat cag ctg att gac att tct gaa 346
Val Pro His Val Asn Arg Thr Asp Tyr Gln Leu Ile Asp Ile Ser Glu
85 90 95

gat gga tat gtc agt ttg ttg act gat aac ggt agt acc aag gat gac 394
Asp Gly Tyr Val Ser Leu Leu Thr Asp Asn Gly Ser Thr Lys Asp Asp
100 105 110

ctt aag ctc cct aat gat gac act ctg ctc caa cag atc aag agt ggg 442
Leu Lys Leu Pro Asn Asp Asp Thr Leu Leu Gln Gln Ile Lys Ser Gly
115 120 125

ttt gat gat gga aaa gat cta gtg gtg agt gta atg tca gct atg gga 490
Phe Asp Asp Gly Lys Asp Leu Val Val Ser Val Met Ser Ala Met Gly
130 135 140 145

gag gaa cag atc aat gct ctt aag gac atc ggt ccc aag tgagactaac 539
Glu Glu Gln Ile Asn Ala Leu Lys Asp Ile Gly Pro Lys
150 155

aaagcctccc ctttgttatg agattcttct tcttctgtag gcttccatta ctcgtcggag 599

attatcttgt ttttgggtta ctcctatctt ggatatttaa acttttggtta ataatgccat 659

cttcttcaac cttttccttc tagatggttt ttatacttct tct 702

<210> 16
 <211> 158
 <212> PRT
 <213> Arabidopsis sp.

<220>
 <223> eif-5A

<400> 16
 Met Ser Asp Glu Glu His His Phe Glu Ser Ser Asp Ala Gly Ala Ser
 1 5 10 15
 Lys Thr Tyr Pro Gln Gln Ala Gly Thr Ile Arg Lys Asn Gly Tyr Ile
 20 25 30
 Val Ile Lys Asn Arg Pro Cys Lys Val Val Glu Val Ser Thr Ser Lys
 35 40 45
 Thr Gly Lys His Gly His Ala Lys Cys His Phe Val Ala Ile Asp Ile
 50 55 60
 Phe Thr Ser Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His Asn Cys
 65 70 75 80
 Asp Val Pro His Val Asn Arg Thr Asp Tyr Gln Leu Ile Asp Ile Ser
 85 90 95
 Glu Asp Gly Tyr Val Ser Leu Leu Thr Asp Asn Gly Ser Thr Lys Asp
 100 105 110
 Asp Leu Lys Leu Pro Asn Asp Asp Thr Leu Leu Gln Gln Ile Lys Ser
 115 120 125
 Gly Phe Asp Asp Gly Lys Asp Leu Val Val Ser Val Met Ser Ala Met
 130 135 140
 Gly Glu Glu Gln Ile Asn Ala Leu Lys Asp Ile Gly Pro Lys
 145 150 155

<210> 17
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 17
 aaarrycgmc cytgcaaggt

20

<210> 18
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 18
 aatacgactc actatag

17

<210> 19
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<220>
 <223> "n" bases represent a, t, c, g, other or unknown

<400> 19
 tcyttncct cmkctaahcc 20

<210> 20
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 20
 attaacctc actaaag 17

<210> 21
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 21
 ctgttaccaa aaaatctgta cc 22

<210> 22
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 22
 agaagaagta taaaaccat c 21

<210> 23
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 23
 aaagaatcct agagagagaa agg 23

<210> 24
 <211> 18
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 24

ttttacatca atcgaaaa

18

<210> 25

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 25

accaaaacct gtgttataac tcc

23

<210> 26

<211> 581

<212> DNA

<213> Arabidopsis sp.

<220>

<223> DHS

<220>

<221> CDS

<222> (1)..(579)

<400> 26

ggt ggt gtt gag gaa gat ctc ata aaa tgc ctt gca cct aca ttt aaa 48
Gly Gly Val Glu Glu Asp Leu Ile Lys Cys Leu Ala Pro Thr Phe Lys
1 5 10 15

ggt gat ttc tct cta cct gga gct tat tta agg tca aag gga ttg aac 96
Gly Asp Phe Ser Leu Pro Gly Ala Tyr Leu Arg Ser Lys Gly Leu Asn
20 25 30

cga att ggg aat ttg ctg gtt cct aat gat aac tac tgc aag ttt gag 144
Arg Ile Gly Asn Leu Leu Val Pro Asn Asp Asn Tyr Cys Lys Phe Glu
35 40 45

gat tgg atc att ccc atc ttt gac gag atg ttg aag gaa cag aaa gaa 192
Asp Trp Ile Ile Pro Ile Phe Asp Glu Met Leu Lys Glu Gln Lys Glu
50 55 60

gag aat gtg ttg tgg act cct tct aaa ctg tta gca cgg ctg gga aaa 240
Glu Asn Val Leu Trp Thr Pro Ser Lys Leu Leu Ala Arg Leu Gly Lys
65 70 75 80

gaa atc aac aat gag agt tca tac ctt tat tgg gca tac aag atg aat 288
Glu Ile Asn Asn Glu Ser Ser Tyr Leu Tyr Trp Ala Tyr Lys Met Asn
85 90 95

att cca gta ttc tgc cca ggg tta aca gat ggc tct ctt agg gat atg 336
Ile Pro Val Phe Cys Pro Gly Leu Thr Asp Gly Ser Leu Arg Asp Met
100 105 110

ctg tat ttt cac tct ttt cgt acc tct ggc ctc atc atc gat gta gta 384
Leu Tyr Phe His Ser Phe Arg Thr Ser Gly Leu Ile Ile Asp Val Val
115 120 125

caa gat atc aga gct atg aac ggc gaa gct gtc cat gca aat cct aaa	432
Gln Asp Ile Arg Ala Met Asn Gly Glu Ala Val His Ala Asn Pro Lys	
130 135 140	
aag aca ggg atg ata atc ctt gga ggg ggc ttg cca aag cac cac ata	480
Lys Thr Gly Met Ile Ile Leu Gly Gly Gly Leu Pro Lys His His Ile	
145 150 155 160	
tgt aat gcc aat atg atg cgc aat ggt gca gat tac gct gta ttt ata	528
Cys Asn Ala Asn Met Met Arg Asn Gly Ala Asp Tyr Ala Val Phe Ile	
165 170 175	
aac acc ggg caa gaa ttt gat ggg agc gac tcg ggt gca cgc cct gat	576
Asn Thr Gly Gln Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp	
180 185 190	
gaa gc	581
Glu	
<210> 27	
<211> 522	
<212> DNA	
<213> Dianthus sp.	
<220>	
<223> DHS	
<220>	
<221> CDS	
<222> (3)..(521)	
<400> 27	
ga aga tcc atc aag tgc ctt gca ccc act ttc aaa ggc gat ttt gcc	47
Arg Ser Ile Lys Cys Leu Ala Pro Thr Phe Lys Gly Asp Phe Ala	
1 5 10 15	
tta cca gga gct caa tta cgc tcc aaa ggg ttg aat cga att ggt aat	95
Leu Pro Gly Ala Gln Leu Arg Ser Lys Gly Leu Asn Arg Ile Gly Asn	
20 25 30	
ctg ttg gtt ccg aat gat aac tac tgt aaa ttt gag gat tgg atc att	143
Leu Leu Val Pro Asn Asp Asn Tyr Cys Lys Phe Glu Asp Trp Ile Ile	
35 40 45	
cca att tta gat aag atg ttg gaa gag caa att tca gag aaa atc tta	191
Pro Ile Leu Asp Lys Met Leu Glu Glu Gln Ile Ser Glu Lys Ile Leu	
50 55 60	
tgg aca cca tcg aag ttg att ggt cga tta gga aga gaa ata aac gat	239
Trp Thr Pro Ser Lys Leu Ile Gly Arg Leu Gly Arg Glu Ile Asn Asp	
65 70 75	
gag agt tca tac ctt tac tgg gcc ttc aag aac aat att cca gta ttt	287
Glu Ser Ser Tyr Leu Tyr Trp Ala Phe Lys Asn Asn Ile Pro Val Phe	
80 85 90 95	
tgc cca ggt tta aca gac ggc tca ctc gga gac atg cta tat ttt cat	335
Cys Pro Gly Leu Thr Asp Gly Ser Leu Gly Asp Met Leu Tyr Phe His	
100 105 110	
tct ttt cgc aat ccg ggt tta atc atc gat gtt gtg caa gat ata aga	383
Ser Phe Arg Asn Pro Gly Leu Ile Ile Asp Val Val Gln Asp Ile Arg	
115 120 125	
gca gta aat ggc gag gct gtg cac gca gcg cct agg aaa aca ggc atg	431

Ala Val Asn Gly Glu Ala Val His Ala Ala Pro Arg Lys Thr Gly Met
 130 135 140

att ata ctc ggt gga ggg ttg cct aag cac cac atc tgc aac gca aac 479
 Ile Ile Leu Gly Gly Gly Leu Pro Lys His His Ile Cys Asn Ala Asn
 145 150 155

atg atg aga aat ggc gcc gat tat gct gtt ttc atc aac acc g 522
 Met Met Arg Asn Gly Ala Asp Tyr Ala Val Phe Ile Asn Thr
 160 165 170

<210> 28
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 28
 ttgargaaga tycatmaat gcct 24

<210> 29
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 29
 ccatcaaayt cytgkgcrgt gtt 23

<210> 30
 <211> 484
 <212> DNA
 <213> Arabidopsis sp.

<220>
 <223> DHS

<220>
 <221> CDS
 <222> (2)..(112)

<400> 30
 t gca cgc cct gat gaa gct gtg tct tgg ggt aaa att agg ggt tct gct 49
 Ala Arg Pro Asp Glu Ala Val Ser Trp Gly Lys Ile Arg Gly Ser Ala
 1 5 10 15

aaa acc gtt aag gtc tgc ttt tta att tct tca cat cct aat tta tat 97
 Lys Thr Val Lys Val Cys Phe Leu Ile Ser Ser His Pro Asn Leu Tyr
 20 25 30

ctc act cag tgg ttt tgagtacata tttaatatgg gatcattctt gcaggtatac 152
 Leu Thr Gln Trp Phe
 35

tgtgatgcta ccatagcctt occattgttg gttgcagaaa catttgccac aaagagagac 212
 caaacctgtg agtctaagac ttaagaactg actgggtcgtt ttggccatgg attcttaaag 272
 atcggttgctt tttgatttta cactggagtg accatataac actccacatt gatgtggctg 332

tgacgcgaat tgtcttcttg cgaattgtac tttagtttct ctcaacctaa aatgatttgc 392
 agattgtggt ttcgtttaaa acacaagagt cttgtagtca ataatocttt gccttataaa 452
 attattcagt tccaacaaaa aaaaaaaaaa aa 484

<210> 31
 <211> 559
 <212> DNA
 <213> Lycopersicon sp.

<220>
 <223> DHS

<220>
 <221> CDS
 <222> (1)..(156)

<220>
 <223> "n" bases represent a, t, c, g, other or unknown

<400> 31
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 Gly Ala Arg Pro Asp Glu Ala Val Ser Trp Gly Lys Ile Arg Gly Gly
 1 5 10 15
 gcc aag act gtg aag gtg cat tgt gat gca acc att gca ttt ccc ata 96
 Ala Lys Thr Val Lys Val His Cys Asp Ala Thr Ile Ala Phe Pro Ile
 20 25 30
 tta gta gct gag aca ttt gca gct aag agt aag gaa ttc tcc cag ata 144
 Leu Val Ala Glu Thr Phe Ala Ala Lys Ser Lys Glu Phe Ser Gln Ile
 35 40 45
 agg tgc caa gtt tgaacattga ggaagctgtc cttccgacca cacatatgaa 196
 Arg Cys Gln Val
 50
 ttgctagctt ttgaagccaa cttgctagtgtg tgcagcacca tttattctgc aaaactgact 256
 agagagcagg gtatatctct ctaccccgag ttagacgaca tctgttatgg ttcaaattaa 316
 ttatttttct ccccttcaca ccatgttatt tagttctctt cctcttcgaa agtgaagagc 376
 ttagatgttc atagggttttg aattatgttg gaggttggtg ataactgact agtcctotta 436
 ccatatagat aatgtatcct tgtactatga gattttgggt gtgtttgata ccaaggaaaa 496
 atgtttattt ggaaaacaat tggattttta atttaaaaaa aattgnttaa aaaaaaaaaa 556
 aaa 559

<210> 32
 <211> 193
 <212> PRT
 <213> Arabidopsis sp.

<220>
 <223> DHS

<400> 32
 Gly Gly Val Glu Glu Asp Leu Ile Lys Cys Leu Ala Pro Thr Phe Lys
 1 5 10 15

[illegible]

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<400> 33
Arg Ser Ile Lys Cys Leu Ala Pro Thr Phe Lys Gly Asp Phe Ala Leu
  1           5           10           15
Pro Gly Ala Gln Leu Arg Ser Lys Gly Leu Asn Arg Ile Gly Asn Leu
          20           25           30
Leu Val Pro Asn Asp Asn Tyr Cys Lys Phe Glu Asp Trp Ile Ile Pro
          35           40           45
Ile Leu Asp Lys Met Leu Glu Glu Gln Ile Ser Glu Lys Ile Leu Trp
      50           55           60
Thr Pro Ser Lys Leu Ile Gly Arg Leu Gly Arg Glu Ile Asn Asp Glu
  65           70           75           80
Ser Ser Tyr Leu Tyr Trp Ala Phe Lys Asn Asn Ile Pro Val Phe Cys
          85           90           95
Pro Gly Leu Thr Asp Gly Ser Leu Gly Asp Met Leu Tyr Phe His Ser
          100          105          110

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Phe Arg Asn Pro Gly Leu Ile Ile Asp Val Val Gln Asp Ile Arg Ala
115 120 125

Val Asn Gly Glu Ala Val His Ala Ala Pro Arg Lys Thr Gly Met Ile
130 135 140

Ile Leu Gly Gly Gly Leu Pro Lys His His Ile Cys Asn Ala Asn Met
145 150 155 160

Met Arg Asn Gly Ala Asp Tyr Ala Val Phe Ile Asn Thr
165 170

<210> 34
<211> 37
<212> PRT
<213> Arabidopsis sp.

<220>
<223> DHS

<400> 34
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Leu Thr Gln Trp Phe
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Ala Lys Thr Val Lys Val His Cys Asp Ala Thr Ile Ala Phe Pro Ile
20 25 30

Leu Val Ala Glu Thr Phe Ala Ala Lys Ser Lys Glu Phe Ser Gln Ile
35 40 45

Arg Cys Gln Val
50